



#13/4B

SEQUENCE LISTING

<110> Cap Daniel
Ferrara, Pascual
Laurent, Patrick
Vita, Natalio

<120> IL-13 RECEPTOR

<130> IVD924

<140> 09/077,817

<141> 1998-09-14

<150> PCT/FR96/01756

<151> 1996-11-07

<160> 15

<170> PatentIn Ver. 2.0

<210> 1

<211> 1539

<212> DNA

<213> Homo sapiens

<400> 1

GGTGCCTGTC GCGGGGAG GAGGCAATAT CAAGGTTTTA AATCTCGGAG AAATGGCTTA 60
ATTCGTTTGC TTGGCTATCG GATGCTTATA TACCTTTCTG ATAAGCACAA CATTGGCTG 120
TACAAGCTTT TGAAGCTTCAT CTTCAGACAC CGAGATAAAA GTTAACCCTC CTCAGGATTT 180
TGAGATAGTG GATTATGAAG AGAACCCGGA TAGTTAGGTT ATCTCTATTT GCAATGGCAA 240
CCCCACTGT CTCTGGATCA TTTTGTGTTG TGAAAGGAAT GCACAGTGGA ATATGAACTA 300
AAATACCGAA ACATTGGTAG TGAAACATGG AAGGCTAGTG TAGAGGTTAC CATCATTACT 360
AAGAATCTAC ATTACAAAGA TGGGTTTGAT CTTAACAAGG GCATTGAATT ATAGAAGGGC 420
GAAGATACAC ACGCTTTTAC CATGGCAATG CACAAATGGA TCAGAAGTTC AAAGTTCCAA 480
TTGCTAGGAG TGGGCAGAAA CTACTTATTG GATATCACCA CAAGGAATTC CAGAACTAA 540
AGTTCAGGAT TAAGTTTTGG GTAGAATGGA TTGCGTATAT TACAATTGGC AATATTTACT 600
CTGTTCTTGG AAACCTGGCA TAGGTTACAT TATGTCTGGG TACTTCTTGA TACCAATTAC 660
AACTTGTTTT ACTGGTATGA GGGCTTGGAT CATGCATTAA ATATATTTGG AAACAGTGTG 720
TTGATTACAT CAAGGCTGAT GGACAAAATA TAGGATGCAG ATTTCCCTAT TTGGCAATAA 780
AGGAGCAGTG AGGCATCAGA CTATAAAGAT TTCTATATTT GTGTTAATGG ATCATCAGAG 840
AACAAGCCTG AAATATCAAG GAATCAGATC CAGTTATTTT ACTTTTCAGC TTCAAAATAT 900
AGTTAAACCT TTGCCGCCAG TCAGTTGGAA ATATCTTACT TTTACTCGGG AGAGTTCATG 960
TGAAATTAAG CTGAAATGGA GCATACCTTT GTTTAGGCGT GGACCTATTC CAGCAAGGTG 1020

TTTTGAATTAT GAAATTGAGA TCAGAGAAGA TGATACTACC GAAAGCATGG AGGAATTTTG 1080
 GTGACTGCTA CAGTTGAAAA TGAAACATAC ACCTTGAAAA CAACAAATGA AACCCGAATA 1140
 ATAGAGTTTT TAGTAGCAAT TATGCTTTGT AGTAAGAAGC AAAGTGAATA TTTATTGCTC 1200
 AGATGACGGA ATTTGGGCAA AGAATCAAGT AGTGAGTGGA GTGATAAACA ATGCTGGGAA 1260
 GGTGAAGACC TATCGAAGAA AACTTTGCTA GTAGCTGGGA TCGTTTCTGG CTACCATTG 1320
 GTTTCATCTT AATATTAGTT ATATTTGTAA CCGGTCTGCT TAGTGAATGT TGCCTAAGCC 1380
 AAACACCTAC CCAAAAATGA TTCCAGAATT TTTCTGTGAT ACATGAAGAA GATTTCATC 1440
 TTTCCATATC AAGAGACATG GTATTGACTC AACAGTTTCC AGTCATGGCC AAATGTTCAA 1500
 TATGAGTCTC AATAAACTGA ATTTTCTTG CGAATGTTG 1539

<210> 2
 <211> 380
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
 1 5 10 15
 Ser Thr Thr Phe Gly Cys Thr Ser Ser Asp Thr Glu Ile Lys Val
 20 25 30
 Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
 35 40 45
 Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
 50 55 60
 Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
 65 70 75 80
 Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
 85 90 95
 Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
 100 105 110
 Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
 115 120 125
 Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
 130 135 140
 Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
 145 150 155 160
 Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
 165 170 175
 Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
 180 185 190
 Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
 195 200 205
 Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
 210 215 220
 Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
 225 230 235 240
 Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
 245 250 255
 Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
 260 265 270

July
 7, 1971

Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
 275 280 285
 Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
 290 295 300
 Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
 305 310 315 320
 Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
 325 330 335
 Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
 340 345 350
 Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
 355 360 365
 Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
 370 375 380

<210> 3

<211> 4009

<212> DNA

<213> Homo sapiens

<400> 3

TCAGCCCGGC CGGGCTCCGA GCGGAGAGGC TGCATGGAGT GGCCGGCGCG GCTCTGCGGG 60
 CTGTGGGCGC TGCTGCTCTG CGCGGGCGGC GGGGGCGGGG GCGGGGCGC CGCGCCTACG 120
 GAAACTCAGC CACCTGTGAC AAATTGAGT GTCTCTGTTG AAAACCTCTG CACAGTAATA 180
 TGGACATGGA ATCCACCCGA GGGAGCCAGC TCAAATTGTA GTCTATGGTA TTTTAGTCAT 240
 TTTGGCGACA AACAAAGATAA GAAATAGCT CCGGAAACTC GTCGTTCAAT AGAAGTACCC 300
 CTGAATGAGA GGATTTGTCT GCAAGTGGGG TCCCAGTGTA GCACCAATGA GAGTGAGAAG 360
 CCTAGCATTT TGGTTGAAAA ATGCATCTCA CCCCCAGAAG GTGATCCTGA GTCTGCTGTG 420
 ACTGAGCTTC AATGCATTTG GCACAACCTG AGCTACATGA AGTGTCTTG GCTCCCTGGA 480
 AGGAATACCA GTCCCGACAC TAACTATACT CTCTACTATT GGCACAGAAG CCTGGAAAAA 540
 ATTCATCAAT GTGAAAACAT CTTTAGAGAA GGCCAATACT TTGGTTGTTC CTTTGATCTG 600
 ACCAAAGTGA AGGATTCCAG TTTTGAACAA CACAGTGTCC AAATAATGGT CAAGGATAAT 660
 GCAGGAAAAA TTAAACCATC CTTCAATATA GTGCCTTTAA CTTCCCGTGT GAAACCTGAT 720
 CCTCCACATA TTAAAAACCT CTCCTTCCAC AATGATGACC TATATGTGCA ATGGGAGAAT 780
 CCACAGAATT TTATTAGCAG ATGCCTATTT TATGAAGTAG AAGTCAATAA CAGCCAAACT 840
 GAGACACATA ATGTTTTCTA CGTCCAAGAG GCTAAATGTG AGAATCCAGA ATTTGAGAGA 900
 AATGTGGAGA ATACATCTTG TTTCATGGTC CCTGGTGTTC TTCCTGATAC TTTGAACACA 960
 GTCAGAATAA GAGTCAAAAC AAATAAGTTA TGCTATGAGG ATGACAAACT CTGGAGTAAT 1020
 TGGAGCCAAG AAATGAGTAT AGGTAAGAAG CGCAATTCCA CACTCTACAT AACCATGTTA 1080
 CTCATTGTTC CAGTCATCGT CGCAGGTGCA ATCATAGTAC TCCTGCTTTA CCTAAAAAGG 1140

Sub
 3,
 cont

CTCAAGATTA TTATATTCCC TCCAATTCCT GATCCTGGCA AGATTTTAA AGAAATGTTT 1200
 GGAGACCAGA ATGATGATAC TCTGCACTGG AAGAAGTACG ACATCTATGA GAAGCAAACC 1260
 AAGGAGGAAA CCGACTCTGT AGTGCTGATA GAAAACCTGA AGAAAGCCTC TCAGTGATGG 1320
 AGATAATTTA TTTTACCTT CACTGTGACC TTGAGAAGAT TCTTCCCATT CTCCATTTGT 1380
 TATCTGGGAA CTTATTAAAT GGAAACTGAA ACTACTGCAC CATTTAAAAA CAGGCAGCTC 1440
 ATAAGAGCCA CAGGTCTTTA TGTTGAGTCG CGCACCGAAA AACTAAAAAT AATGGGCGCT 1500
 TTGGAGAAGA GTGTGGAGTC ATTCTCATTG AATTATAAAA GCCAGCAGGC TTCAAAC TAG 1560
 GGGACAAAGC AAAAAGTGAT GATAGTGGTG GAGTTAATCT TATCAAGAGT TGTGACAACT 1620
 TCCTGAGGGA TCTATACCTG CTTTGTGTTT TTTGTGTCAA CATGAACAAA TTTTATTTGT 1680
 AGGGGAACTC ATTTGGGGTG CAAATGCTAA TGTCAAACCT GAGTCACAAA GAACATGTAG 1740
 AAAACAAAAT GGATAAAATC TGATATGTAT TGTTTGGGAT CCTATTGAAC CATGTTTGTG 1800
 GCTATTAAAA CTCTTTTAACT AGTCTGGGCT GGGTCCGGTG GCTCACGCCT GTAATCCCAG 1860
 CAATTTGGGA GTCCGAGGCG GCGGATCAC TCGAGGTCAG GAGTTCCAGA CCAGCCTGAC 1920
 CAAAATGGTG AAACCTCCTC TCTACTAAAA CTACAAAAAT TAACTGGGTG TGGTGGCGCG 1980
 TGCCTGTAAT CCCAGCTACT CGGGAAGCTG AGGCAGGTGA ATTGTTTGAA CCTGGGAGGT 2040
 GGAGGTTGCA GTGAGCAGAG ATCACACCAC TGCACTCTAG CCTGGGTGAC AGAGCAAGAC 2100
 TCTGTCTAAA AAACAAAACA AAACAAAACA AAACAAAAAA ACCTCTTAAT ATTCTGGAGT 2160
 CATCATTCCC TTCGACAGCA TTTTCCTCTG CTTTGAAAGC CCCAGAAATC AGTGTTGGCC 2220
 ATGATGACAA CTACAGAAAA ACCAGAGGCA GGTTCCTTGC CAAGACCTTT CAAAGCCATT 2280
 TTAGGCTGTT AGGGGCAGTG GAGGTAGAAT GACTCCTTGG GTATTAGAGT TTCAACCATG 2340
 AAGTCTCTAA CAATGTATTT TCTTCACCTC TGCTACTCAA GTAGCATTTA CTGTGTCTTT 2400
 GGTGTGTGCT AGGCCCCCGG GTGTGAAGCA CAGACCCCTT CCAGGGGTTT ACAGTCTATT 2460
 TGAGACTCCT CAGTTCTTGC CACTTTTTTT TTTAATCTOC ACCAGTCATT TTTCAGACCT 2520
 TTTAACTCCT CAATTCCAAC ACTGATTTCC CCTTTTGCAT TCTCCCTCCT TCCCTTCCTT 2580
 GTAGCCTTTT GACTTTCATT GGAAATTAGG ATGTAAATCT GCTCAGGAGA CCTGGAGGAG 2640
 CAGAGGATAA TTAGCATCTC AGGTAAAGTG TGAGTAATCT GAGAAACAAT GACTAATTCT 2700
 TGCATATTTT GTAACCTCCA TGTGAGGGTT TTCAGCATTG ATATTGTGC ATTTTCTAAA 2760
 CAGAGATGAG GTGGTATCTT CACGTAGAAC ATTGGTATTC GCTTGAGAAA AAAAGAATAG 2820
 TTGAACCTAT TTCTCTTTCT TTACAAGATG GGTCCAGGAT TCCTCTTTTC TCTGCCATAA 2880
 ATGATTAATT AAATAGCTTT TGTGTCTTAC ATTGGTAGCC AGCCAGCCAA GGCTCTGTTT 2940
 ATGCTTTTGG GGGGCATATA TTGGGTTCCTA TTCTCACCTA TCCACACAAC ATATCCGTAT 3000

Sub
 31
 done

ATATCCCCTC TACTCTTACT TCCCCCAAAT TTAAAGAAGT ATGGGAAATG AGAGGCATTT 3060
 CCCCCACCCC ATTTCTCTCC TCACACACAG ACTCATATTA CTGGTAGGAA CTTGAGAACT 3120
 TTATTTCCAA GTTGTTCAAA CATTTACCAA TCATATTAAT ACAATGATGC TATTTGCAAT 3180
 TCCTGCTCCT AGGGGAGGGG AGATAAGAAA CCCTCACTCT CTACAGGTTT GGGTACAAGT 3240
 GGCAACCTGC TTCCATGGCC GTGTAGAAGC ATGGTGCCCT GGCTTCTCTG AGGAAGCTGG 3300
 GGTTTCATGAC AATGGCAGAT GTAAAGTTAT TCTTGAAGTC AGATTGAGGC TGGGAGACAG 3360
 CCGTAGTAGA TGTTCTACTT TGTTCTGCTG TTCTCTAGAA AGAATATTTG GTTTTCCTGT 3420
 ATAGGAATGA GATTAATTC TTTCCAGGTA TTTTATAATT CTGGGAAGCA AAACCCATGC 3480
 CTCCCCCTAG CCATTTTTC TGTTATCCTA TTTAGATGGC CATGAAGAGG ATGCTGTGAA 3540
 ATTCCCAACA AACATTGATG CTGACAGTCA TGCAGTCTGG GAGTGGGGAA GTGATCTTTT 3600
 GTTCCCATCC TCTTCTTTTA GCAGTAAAT AGCTGAGGGA AAAGGGAGGG AAAAGGAAGT 3660
 TATGGGAATA CCTGTGGTGG TTGTGATCCC TAGGTCTTGG GAGCTCTTGG AGGTGTCTGT 3720
 ATCAGTGGAT TTCCCATCCC CTGTGGGAAA TTAGTAGGCT CATTTACTGT TTAGGTCTA 3780
 GCCTATGTGG ATTTTTTCCT AACATACCTA AGCAAACCCA GTGTCAGGAT GGTAATTCTT 3840
 ATTCTTTCGT TCAGTTAAGT TTTTCCCTTC ATCTGGGCAC TGAAGGGATA TGTGAAACAA 3900
 TGTTAACATT TTTGGTAGTC TTCAACCAGG GATTGTTTCT GTTTAACTTC TTATAGGAAA 3960
 GCTTGAGTAA AATAAATATT GTCTTTTGT ATGTCACCCA AAAAAAAAAA 4009

<210> 4
 <211> 427
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
 1 5 10 15
 Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln
 20 25 30
 Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val
 35 40 45
 Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu
 50 55 60
 Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro
 65 70 75 80
 Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu
 85 90 95
 Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile
 100 105 110
 Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala
 115 120 125
 Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys

130 135 140
 Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu
 145 150 155 160
 Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile
 165 170 175
 Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val
 180 185 190
 Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp
 195 200 205
 Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser
 210 215 220
 Arg Val Lys Pro Asp Pro His Ile Lys Asn Leu Ser Phe His Asn
 225 230 235 240
 Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg
 245 250 255
 Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His
 260 265 270
 Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu
 275 280 285
 Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro
 290 295 300
 Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys
 305 310 315 320
 Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile
 325 330 335
 Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val
 340 345 350
 Pro Val Ile Val Ala Gly Ala Ile Val Leu Leu Leu Tyr Leu Lys
 355 360 365
 Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile
 370 375 380
 Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys
 385 390 395 400
 Lys Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val
 405 410 415
 Val Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
 420 425

<210> 5
 <211> 420
 <212> PRT
 <213> Homo sapiens

<400> 5

Met Ile Ile Val Ala His Val Leu Leu Ile Leu Leu Gly Ala Thr Glu
 1 5 10 15
 Ile Leu Gln Ala Asp Leu Leu Pro Asp Glu Lys Ile Ser Leu Leu Pro
 20 25 30
 Pro Val Asn Phe Thr Ile Lys Val Thr Gly Leu Ala Gln Val Leu Leu
 35 40 45
 Gln Trp Lys Pro Asn Pro Asp Gln Glu Gln Arg Asn Val Asn Leu Glu
 50 55 60
 Tyr Gln Val Lys Ile Asn Ala Pro Lys Glu Asp Asp Tyr Glu Thr Arg
 65 70 75 80
 Ile Thr Glu Ser Lys Cys Val Thr Ile Leu His Lys Gly Phe Ser Ala
 85 90 95
 Ser Val Arg Thr Ile Leu Gln Asn Asp His Ser Leu Leu Ala Ser Ser
 100 105 110

Due
 31
 Cont

Trp Ala Ser Ala Glu Leu His Ala Pro Pro Gly Ser Pro Gly Thr Ser
 115 120 125
 Ile Val Asn Leu Thr Cys Thr Thr Asn Thr Thr Glu Asp Asn Tyr Ser
 130 135 140
 Arg Leu Arg Ser Tyr Gln Val Ser Leu His Cys Thr Trp Leu Val Gly
 145 150 155 160
 Thr Asp Ala Pro Glu Asp Thr Gln Tyr Phe Leu Tyr Tyr Arg Tyr Gly
 165 170 175
 Ser Trp Thr Glu Glu Cys Gln Glu Tyr Ser Lys Asp Thr Leu Gly Arg
 180 185 190
 Asn Ile Ala Cys Trp Phe Pro Arg Thr Phe Ile Leu Ser Lys Gly Arg
 195 200 205
 Asp Trp Leu Ser Val Leu Val Asn Gly Ser Ser Lys His Ser Ala Ile
 210 215 220
 Arg Pro Phe Asp Gln Leu Phe Ala Leu His Ala Ile Asp Gln Ile Asn
 225 230 235 240
 Pro Pro Leu Asn Val Thr Ala Glu Ile Glu Gly Thr Arg Leu Ser Ile
 245 250 255
 Gln Trp Glu Lys Pro Val Ser Ala Phe Pro Ile His Cys Phe Asp Tyr
 260 265 270
 Glu Val Lys Ile His Asn Thr Arg Asn Gly Tyr Leu Gln Ile Glu Lys
 275 280 285
 Leu Met Thr Asn Ala Phe Ile Ser Ile Ile Asp Asp Leu Ser Lys Tyr
 290 295 300
 Asp Val Gln Val Arg Ala Ala Val Ser Ser Met Cys Arg Glu Ala Gly
 305 310 315 320
 Leu Trp Ser Glu Trp Ser Gln Pro Ile Tyr Val Gly Asn Asp Glu His
 325 330 335
 Lys Pro Leu Arg Glu Trp Phe Val Ile Val Ile Met Ala Thr Ile Cys
 340 345 350
 Phe Ile Leu Leu Ile Leu Ser Leu Ile Cys Lys Ile Cys His Leu Trp
 355 360 365
 Ile Lys Leu Phe Pro Pro Ile Pro Ala Pro Lys Ser Asn Ile Lys Asp
 370 375 380
 Leu Phe Val Thr Thr Asn Tyr Glu Lys Ala Gly Ser Ser Glu Thr Glu
 385 390 395 400
 Ile Glu Val Ile Cys Tyr Ile Glu Lys Pro Gly Val Glu Thr Leu Glu
 405 410 415
 Asp Ser Val Phe
 420

<210> 6
 <211> 424
 <212> PRT
 <213> Mus musculus

<400> 6

Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
 1 5 10 15
 Thr Ala Thr Val Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro Pro
 20 25 30
 Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile Trp
 35 40 45
 Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr

Sub
 41
 cont

50 55 60
 Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu Thr
 65 70 75 80
 His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln Val
 85 90 95
 Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu Val
 100 105 110
 Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Arg Glu Ser Ala Val Thr
 115 120 125
 Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp
 130 135 140
 Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr Tyr
 145 150 155 160
 Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr Arg
 165 170 175
 Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro
 180 185 190
 Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly
 195 200 205
 Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr Val Lys
 210 215 220
 Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly Ala Leu
 225 230 235 240
 Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr
 245 250 255
 Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn Ile Leu
 260 265 270
 Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg Asn Met
 275 280 285
 Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp Ala Val
 290 295 300
 Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe Asp Asp
 305 310 315 320
 Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly Lys Glu
 325 330 335
 Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro Val Phe
 340 345 350
 Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg Leu Lys
 355 360 365
 Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu
 370 375 380

Sub
 31
 cont

Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp
 385 390 395 400

Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val Leu Ile
 405 410 415

Glu Asn Leu Lys Lys Ala Ala Pro
 420

<210> 7
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 7

AGAGGAATTA CCCCTGGATG 20

<210> 8
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> anti-sense primer

<400> 8

TCAAGGAGCT GCTTTCTTCA 20

<210> 9
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 9

GATCCACTTC CCAAGAACAG A 21

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 10

GATCCGGGCC CTTTTTTTTT TTT 23

<210> 11
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> in SEQ ID NO. 12, which is a variant of SEQ ID NO. 2, the sequence VRCVTL is substituted for the 8 C-terminal amino acids of the human protein.

<400> 11
 Val Arg Cys Val Thr Leu
 1 5

<210> 12
 <211> 378
 <212> PRT
 <213> Artificial sequence

<220>
 <223> variant of SEQ ID NO. 2 in which the sequence VRCVTL is substituted for the 8 C-terminal amino acids of the human protein.

<400> 12

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
 1 5 10 15
 Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
 20 25 30
 Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
 35 40 45
 Leu Tyr Leu Gln Trp Gln Pro Leu Ser Leu Asp His Phe Lys Glu
 50 55 60
 Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
 65 70 75 80
 Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
 85 90 95
 Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
 100 105 110
 Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
 115 120 125
 Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
 130 135 140
 Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
 145 150 155 160
 Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
 165 170 175
 Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
 180 185 190
 Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
 195 200 205
 Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
 210 215 220
 Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
 225 230 235 240
 Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu

		245					250					255			
Lys	Trp	Ser	Ile	Pro	Leu	Gly	Pro	Ile	Pro	Ala	Arg	Cys	Phe	Asp	Tyr
		260						265					270		
Glu	Ile	Glu	Ile	Arg	Glu	Asp	Asp	Thr	Thr	Leu	Val	Thr	Ala	Thr	Val
		275					280					285			
Glu	Asn	Glu	Thr	Tyr	Thr	Leu	Lys	Thr	Thr	Asn	Glu	Thr	Arg	Gln	Leu
	290					295				300					
Cys	Phe	Val	Val	Arg	Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	Asp	Asp	Gly
305					310					315					320
Ile	Trp	Ser	Glu	Trp	Ser	Asp	Lys	Gln	Cys	Trp	Glu	Gly	Glu	Asp	Leu
			325						330					335	
Ser	Lys	Lys	Thr	Leu	Leu	Arg	Phe	Trp	Leu	Pro	Phe	Gly	Phe	Ile	Leu
			340					345					350		
Ile	Leu	Val	Ile	Phe	Val	Thr	Gly	Leu	Leu	Leu	Arg	Lys	Pro	Asn	Thr
	355					360						365			
Tyr	Pro	Lys	Met	Val	Arg	Cys	Val	Thr	Leu						
	370					375									

<210> 13
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motif characteristic of the family of chemokine receptors to which the polypeptides of SEQ ID NO. 2 and SEQ NO. 4 belong. Xaa can be any amino acid.

<400> 13

Trp Ser Xaa Trp Ser
 1 5

<210> 14
 <211> 6
 <212> DNA
 <213> Artificial sequence

<220>
 <223> polyadenylation signal

<400> 14

AATAAA 6

<210> 15
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 15

AAAAAAAAAA AAAGGGCCCG

20

See Fig 1